



SEQUENCE LISTING

<110> Klock, Andrew P.
Williams, Deryck Jeremy
Salmon, Brandy

<120> NEMATODE GS-LIKE SEQUENCES

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<140> US 10/098,602

<141> 2002-03-15

<150> US 60/276,621

<151> 2001-03-16

<160> 9

<170> FastSEQ for Windows Version 4.0

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<211> 1471

<212> DNA

<213> Meloidogyne incognita

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Leu Asn Asn Leu Ile Arg Asn Gly Lys Ile Asp Thr Val Val Leu Ala		
10 15 20		
tyc gtc gac atg caa ggc cgg ctg atg ggc aag aga tta act ggg cgt	150	
Cys Val Asp Met Gln Gly Arg Leu Met Gly Lys Arg Leu Thr Gly Arg		
25 30 35		
cat ttt tta gga ttg gat caa aag aag att agc att agc acg ttt gta	198	
His Phe Leu Gly Leu Asp Gln Lys Lys Ile Ser Ile Ser Thr Phe Val		
40 45 50 55		
tat gcg gta act ata gaa ggc atc gct ggc gga ggt tat gag atc tca	246	
Tyr Ala Val Thr Ile Glu Gly Ile Ala Gly Gly Gly Tyr Glu Ile Ser		
60 65 70		
agt gta gac aca ggt tat agt gat tgt cat ctc tgt gca gat ttg aat	294	
Ser Val Asp Thr Gly Tyr Ser Asp Cys His Leu Cys Ala Asp Leu Asn		
75 80 85		
tcc ctt cat tta ctc ccg tgg tca gaa ggc gct gta ttg gca att tcc	342	
Ser Leu His Leu Leu Pro Trp Ser Glu Gly Ala Val Leu Ala Ile Ser		

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gta ata ctc atg cag caa att gag cgc ctg gct aat cta aag ctt aaa Val Ile Leu Met Gln Gln Ile Glu Arg Leu Ala Asn Leu Lys Leu Lys 120 125 130 135			438
ggc ctt ttt gct tct gaa cta gaa ttt aat ctt ttc aac gaa act tat Gly Leu Phe Ala Ser Glu Leu Glu Phe Asn Leu Phe Asn Glu Thr Tyr 140 145 150			486
aag agt ggc agc caa aag cat tgg aaa aat tta aaa acc gag cag cct Lys Ser Ala Ser Gln Lys His Trp Lys Asn Leu Lys Thr Ala Gln Pro 155 160 165			534
cat cat caa tgg atg aat att agt gca agt agt ggg att gaa act ttt His His Gln Trp Met Asn Ile Ser Ala Ser Ser Gly Ile Glu Thr Phe 170 175 180			582
atg cgt tct gtg cgt aat aaa tta gaa gaa ggc ggt att ttg atg gag Met Arg Ser Val Arg Asn Lys Leu Glu Glu Ala Gly Ile Leu Met Glu 185 190 195			630
ggg aca cat ccc gaa ttt tta cct agt cag cat gaa ctt aat ttt gta Ala Thr His Pro Glu Phe Leu Pro Ser Gln His Glu Leu Asn Phe Val 200 205 210 215			678
cca gcc gat cct cta aca atg gca gat cgt cat att att gca aaa cat Pro Ala Asp Pro Leu Thr Met Ala Asp Arg His Ile Ile Ala Lys His 220 225 230			726
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tca ctt caa gat gca gaa aca gaa aaa aat gca ttt tat gat caa aac Ser Leu Gln Asp Ala Glu Thr Glu Lys Asn Ala Phe Tyr Asp Gln Asn 265 270 275			870
gat gaa tat gga atg tca acc tta gct cgt aat tgg att gct gga tta Asp Glu Tyr Gly Met Ser Thr Leu Ala Arg Asn Trp Ile Ala Gly Leu 280 285 290 295			918
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tcc gag gga att aat gtt gag ctg cgt att ggt ggc gct gat ttg aac Ser Glu Gly Ile Asn Val Glu Leu Arg Ile Gly Gly Ala Asp Leu Asn 345 350 355	1110
cct tat tta gct ttt tcc gca atc ata gct gca gga att agc ggt ata Pro Tyr Leu Ala Phe Ser Ala Ile Ile Ala Ala Gly Ile Ser Gly Ile 360 365 370 375	1158
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ctt cta aaa gaa tgg aaa atg ctg aat aaa aca ttc ggg gag aag ttg Leu Leu Lys Glu Ser Lys Met Leu Asn Lys Thr Phe Gly Glu Lys Leu 410 415 420	1302
att cta cat tat gta aac gct gct aat gtt gag att aat gaa ttt tca Ile Leu His Tyr Val Asn Ala Ala Asn Val Glu Ile Asn Glu Phe Ser 425 430 435	1350
aaa caa gtt act gac tgg gag ctt aat caa gga ttt aat aga tat Lys Gln Val Thr Asp Trp Glu Leu Asn Gln Gly Phe Asn Arg Tyr 440 445 450	1398
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<211> 454

<212> PRT

<213> Meloidogyne incognita

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Gly Lys Arg Leu Thr Gly Arg His Phe Leu Gly Leu Asp Gln Lys Lys	
35 40 45	
Ile Ser Ile Ser Thr Phe Val Tyr Ala Val Thr Ile Glu Gly Ile Ala	
50 55 60	
Gly Gly Gly Tyr Glu Ile Ser Ser Val Asp Thr Gly Tyr Ser Asp Cys	
65 70 75 80	
His Leu Cys Ala Asp Leu Asn Ser Leu His Leu Leu Pro Trp Ser Glu	
85 90 95	
Gly Ala Val Leu Ala Ile Ser Asn Pro His Asn Phe Val Thr Ser Glu	
100 105 110	
Pro Leu Phe Cys Ser Pro Arg Val Ile Leu Met Gln Gln Ile Glu Arg	

115	120	125
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145	150	155
Asn Leu Lys Thr Ala Gln Pro His His Gln Trp Met Asn Ile Ser Ala		
165	170	175
Ser Ser Gly Ile Glu Thr Phe Met Arg Ser Val Arg Asn Lys Leu Glu		
180	185	190
Glu Ala Gly Ile Leu Met Glu Ala Thr His Pro Glu Phe Leu Pro Ser		
195	200	205
Gln His Glu Leu Asn Phe Val Pro Ala Asp Pro Leu Thr Met Ala Asp		
210	215	220
Arg His Ile Ile Ala Lys His Gly Val Arg Glu Met Ala Glu Gln Ser		
225	230	235
Gly Met Val Ala Thr Phe Met Ala Lys Leu Ser Ser Thr Ala Leu Gly		
245	250	255
Asn Ala Cys His Ile His Met Ser Leu Gln Asp Ala Glu Thr Glu Lys		
260	265	270
Asn Ala Phe Tyr Asp Gln Asn Asp Glu Tyr Gly Met Ser Thr Leu Ala		
275	280	285
Arg Asn Trp Ile Ala Gly Leu Leu Lys Tyr Val Pro Glu Ala Thr Tyr		
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Phe Phe Ala Ser Tyr Ile Asn Ser Tyr Lys Arg Leu Gln Pro Leu Thr		
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Phe Ala Pro Thr Lys Cys Cys Trp Ala Ile Asp Asn Arg Thr Ser Ala		
325	330	335
Phe Arg Leu Cys Asn Ser Lys Ser Glu Gly Ile Asn Val Glu Leu Arg		
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Ile Gly Gly Ala Asp Leu Asn Pro Tyr Leu Ala Phe Ser Ala Ile Ile		
355	360	365
Ala Ala Gly Ile Ser Gly Ile Glu Glu Lys Leu Glu Leu Pro Pro Pro		
370	375	380
Ala Ser Gly Asn Val Tyr Asn Asp Lys Glu Leu Pro Glu Phe Pro Asn		
385	390	395
Ser Leu Gln Asn Ala Thr His Leu Leu Lys Glu Ser Lys Met Leu Asn		
405	410	415
Lys Thr Phe Gly Glu Lys Leu Ile Leu His Tyr Val Asn Ala Ala Asn		
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<C12> DNA

<C13> Meloidogyne incognita

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catctctgtg	cagatttgaa	ttccttccat	taactccgt	ggtcagaagg	cgtctgattg	300
gcaatttcca	atcttcataa	tttctttact	tctgagccat	tgttctgttc	tcctcgagta	360
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<212> PRT

<213> Mycobacterium tuberculosis

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Met Gln Gly Arg Leu Ala Gly Lys Arg Ile Ser Gly Arg His Phe Val
          35          40          45
Asp Asp Ile Ala Thr Arg Gly Val Glu Cys Cys Ser Tyr Leu Leu Ala
          50          55          60
Val Asp Val Asp Leu Asn Thr Val Pro Gly Tyr Ala Met Ala Ser Trp
          65          70          75          80
Asp Thr Gly Tyr Gly Asp Met Val Met Thr Pro Asp Leu Ser Thr Leu
          85          90          95
Arg Leu Ile Pro Trp Leu Pro Gly Thr Ala Leu Val Ile Ala Asp Leu
          100          105          110
Val Trp Ala Asp Gly Ser Glu Val Ala Val Ser Pro Arg Ser Ile Leu
          115          120          125
Arg Arg Gln Leu Asp Arg Leu Lys Ala Arg Gly Leu Val Ala Asp Val
          130          135          140
Ala Thr Glu Leu Glu Phe Ile Val Phe Asp Gln Pro Tyr Arg Gln Ala
          145          150          155          160
Trp Ala Ser Gly Tyr Arg Gly Leu Thr Pro Ala Ser Asp Tyr Asn Ile
          165          170          175
Asp Tyr Ala Ile Leu Ala Ser Ser Arg Met Glu Pro Leu Leu Arg Asp
          180          185          190
Ile Arg Leu Gly Met Ala Gly Ala Gly Leu Arg Phe Glu Ala Val Lys
          195          200          205
Gly Glu Cys Asn Met Gly Gln Gln Glu Ile Gly Phe Arg Tyr Asp Glu
          210          215          220
Ala Leu Val Thr Cys Asp Asn His Ala Ile Tyr Lys Asn Gly Ala Lys
          225          230          235          240
Glu Ile Ala Asp Gln His Gly Lys Ser Leu Thr Phe Met Ala Lys Tyr
          245          250          255
Asp Glu Arg Glu Gly Asn Ser Cys His Ile His Val Ser Leu Arg Gly
          260          265          270

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Thr Asp Gly Ser Ala Val Phe Ala Asp Ser Asn Gly Pro His Gly Met
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 Ser Ser Met Phe Arg Ser Phe Val Ala Gly Gln Leu Ala Thr Leu Arg
 290 295 300
 Glu Phe Thr Leu Cys Tyr Ala Pro Thr Ile Asn Ser Tyr Lys Arg Phe
 305 310 315 320
 Ala Asp Ser Ser Phe Ala Pro Thr Ala Leu Ala Trp Gly Leu Asp Asn
 325 330 335
 Arg Thr Cys Ala Leu Arg Val Val Gly His Gly Gln Asn Ile Arg Val
 340 345 350
 Glu Cys Arg Val Pro Gly Gly Asp Val Asn Gln Tyr Leu Ala Val Ala
 355 360 365
 Ala Leu Ile Ala Gly Gly Leu Tyr Gly Ile Glu Arg Gly Leu Gln Leu
 370 375 380
 Pro Glu Pro Cys Val Gly Asn Ala Tyr Gln Gly Ala Asp Val Glu Arg
 385 390 395 400
 Leu Pro Val Thr Leu Ala Asp Ala Ala Val Leu Phe Glu Asp Ser Ala
 405 410 415
 Leu Val Arg Glu Ala Phe Gly Glu Asp Val Val Ala His Tyr Leu Asn
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<212> DNA

<213> Artificial Sequence

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<223> primer

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